

**AMENDMENTS TO THE CLAIMS**

**This listing of claims will replace all prior versions and listings of claims in the application:**

**LISTING OF CLAIMS:**

1. (currently amended) A method of measuring a chromosome territory, the method detecting a difference in state between a plurality of cells containing a chromosome territory by measuring a desired area of said cells from information obtained from a plurality of images formed from a plurality of pixels having an attribute value, the images being taken of said plurality of cells, the method comprising:

extracting said chromosome territory from an image;

standardizing a positioning state of said chromosome territory and then quantifying said positioning state; and

detecting a difference in state between said cells based on the quantified positioning state of said chromosome territory,

said extracting including:

classifying said image into a plurality of classes; and

extracting any of said classes from said image as a region representing said chromosome territory, and

said classifying including:

setting an initial value for an attribute parameter indicating an attribute value of each of said classes and for a mixture ratio of each of said classes;

|                    calculating, using a processor, based on said attribute parameter and said mixture ratio a class membership probability of each of said plurality of pixels being classified into each of said classes;

|                    calculating, using a processor, an evaluation function representing a goodness of estimation based on said membership probability and a mixture probability distribution defined by said attribute parameter and said mixture ratio and determining whether or not said evaluation function satisfies predetermined conditions;

                  updating said attribute parameter and said mixture ratio when said evaluation function does not satisfy said predetermined conditions; and

                  classifying said plurality of pixels into any of said plurality of classes based on said attribute parameter and said mixture ratio when said evaluation function satisfies said predetermined conditions.

2.        (Original) The measurement method as set forth in Claim 1,  
          wherein in said chromosome territory extraction, in addition to extracting a nucleus of said cell said chromosome territory contained in said nucleus is extracted, and  
          said positioning state quantification comprises standardizing a form of said nucleus and transforming coordinates of said chromosome territory based on a change in form between said nucleus before standardization and said nucleus after standardization.

3.        (Original) The measurement method as set forth in Claim 1 or Claim 2, the method further comprising:

statistically processing quantification results of said positioning state of a plurality of cells,

wherein in said detection of difference in state between cells, a difference in state of a single cell is detected based on a result of quantifying said positioning state of said single cell and a result of said statistical processing.

4. (Original) The detection method as set forth in Claim 3,  
wherein said statistical processing comprises calculating a standard value of a quantification result of said positioning state based on a result of quantifying said positioning state of a plurality of cells, and

in said detection of difference in state between cells, a difference in state of a single cell is detected based on a result of quantifying said positioning state of said single cell and said standard value.

5. (currently amended) A method of measuring a chromosome territory, the method detecting a difference in state between a plurality of cells containing a chromosome territory by measuring a desired area of said cells from information obtained from a plurality of images formed from a plurality of pixels having an attribute value, the images being taken of said plurality of cells, the method comprising:

extracting a plurality of chromosome territories from an image;  
quantifying a positioning state of said plurality of chromosome territories;  
statistically processing results of quantifying said positioning state of a plurality of cells;  
and

detecting a difference in state of a single cell based on a result of quantifying said  
positioning state of said single cell and a result of said statistical processing,

said extracting including:

classifying said image into a plurality of classes; and

extracting any of said classes from said image as a region representing said  
chromosome territory, and

said classifying including:

setting an initial value for an attribute parameter indicating an attribute  
value of each of said classes and for a mixture ratio of each of said classes;

calculating, using a processor, based on said attribute parameter and said  
mixture ratio a class membership probability of each of said plurality of pixels being classified  
into each of said classes;

calculating, using a processor, an evaluation function representing a  
goodness of estimation based on said membership probability and a mixture probability  
distribution defined by said attribute parameter and said mixture ratio and determining whether  
or not said evaluation function satisfies predetermined conditions;

updating said attribute parameter and said mixture ratio when said  
evaluation function does not satisfy said predetermined conditions; and

classifying said plurality of pixels into any of said plurality of classes  
based on said attribute parameter and said mixture ratio when said evaluation function satisfies  
said predetermined conditions.

6. (Original) The measurement method as set forth in Claim 5,

wherein said positioning state comprises at least one of a distance between said plurality of chromosome territories and a positioning direction of said plurality of chromosome territories.

7. (Original) The measurement method as set forth in Claim 5 or 6,  
wherein said quantifying comprises calculating a distance between said plurality of chromosome territories.

8. (Original) The measurement method as set forth in Claim 7,  
wherein said distance calculation comprises:  
calculating a center of gravity of each of said plurality of chromosome territories; and  
calculating a distance between said centers of gravity.

9. (previously presented) The measurement method as set forth in any one of claims 5 or 6,  
wherein said quantifying comprises quantifying a positioning direction of said plurality of chromosome territories.

10. (Original) The measurement method as set forth in Claim 9,  
wherein said positioning direction quantification comprises:  
detecting a principal axis of each of said plurality of chromosome territories; and  
calculating an angle of said principal axis.

11. (currently amended) A method of measuring a chromosome territory, the method detecting a difference in state between a plurality of cells containing a chromosome territory by measuring a desired area of said cells in information of a plurality of images formed from a plurality of pixels having an attribute value, the images being taken of said plurality of cells, the method comprising:

extracting each of a nucleus of said cells and said chromosome territory from said image;

quantifying a positioning state of said nucleus and said chromosome territory;

statistically processing a result of quantifying said positioning state of a plurality of cells;

and

detecting a difference in state of a single cell based on a result of quantifying said positioning state of said single cell and a result of said statistical processing,

said extracting including:

classifying said image into a plurality of classes; and

extracting any of said classes from said image as a region representing said chromosome territory, and

said classifying including:

setting an initial value for an attribute parameter indicating an attribute value of each of said classes and for a mixture ratio of each of said classes;

calculating, using a processor, based on said attribute parameter and said mixture ratio a class membership probability of each of said plurality of pixels being classified into each of said classes;

calculating, using a processor, an evaluation function representing a goodness of estimation based on said membership probability and a mixture probability distribution defined

by said attribute parameter and said mixture ratio and determining whether or not said evaluation function satisfies predetermined conditions;

updating said attribute parameter and said mixture ratio when said evaluation function does not satisfy said predetermined conditions; and

classifying said plurality of pixels into any of said plurality of classes based on said attribute parameter and said mixture ratio when said evaluation function satisfies said predetermined conditions.

12. (Original) The measurement method as set forth in Claim 11,  
wherein said quantifying comprises calculating a distance between a reference point within said nucleus and said chromosome territory.

13. (previously presented): The measurement method as set forth in any one of claims 5, 6, 11 or 12,  
wherein said chromosome territory positioning state quantification further comprises standardizing a positioning state of said chromosome territory, and after standardizing the positioning state of said chromosome territory, quantifying said positioning state.

14. (Original) The measurement method as set forth in Claim 13,  
wherein said statistical processing comprises calculating a standard value of a quantification result of said positioning state based on a result of quantifying said positioning state of a plurality of cells; and

in said detection of difference in state of a single cell, a difference in state of a single cell is detected based on a result of quantifying said positioning state of said single cell and said standard value.

15. (previously presented) The measurement method as set forth in any one of Claims 1, 2, 5, 6, 11 or 12,

wherein said positioning state comprises at least one of a relative position of said chromosome territory within a nucleus of said cell, a direction of a principal axis of said chromosome territory, and a spread of said chromosome territory.

16. (Cancelled).

17. (Original) The measurement method as set forth in Claim 1,  
wherein said class membership probability calculation comprises:

decomposing said plurality of pixels into a plurality of partial spaces according to an attribute value of said pixels;

calculating a coarse-grained empirical probability distribution representing a proportion of pixels contained in said partial space; and

calculating based on said attribute parameter and said mixture ratio a coarse-grained class membership probability of each of said partial spaces being classified into each of said classes; and

said evaluation function calculation comprises calculating a coarse-grained mixture probability distribution by averaging, within said partial space, mixture probability



distributions defined by said attribute parameter and said mixture ratio, said evaluation function being calculated based on said coarse-grained empirical probability distribution, said coarse-grained mixture probability distribution, and said coarse-grained class membership probability.

18-22. (Cancelled).

23. (previously presented) The measurement method as set forth in claim 8, wherein said quantifying comprises quantifying a positioning direction of said plurality of chromosome territories.

24. (previously presented) The measurement method as set forth in claim 8, wherein said chromosome territory positioning state quantification further comprises standardizing a positioning state of said chromosome territory, and after standardizing the positioning state of said chromosome territory, quantifying said positioning state.

25. (previously presented) The measurement method as set forth in claim 10, wherein said chromosome territory positioning state quantification further comprises standardizing a positioning state of said chromosome territory, and after standardizing the positioning state of said chromosome territory, quantifying said positioning state.

26. (previously presented) The measurement method as set forth in Claim 4,

wherein said positioning state comprises at least one of a relative position of said chromosome territory within a nucleus of said cell, a direction of a principal axis of said chromosome territory, and a spread of said chromosome territory.

27. (previously presented) The measurement method as set forth in Claim 8, wherein said positioning state comprises at least one of a relative position of said chromosome territory within a nucleus of said cell, a direction of a principal axis of said chromosome territory, and a spread of said chromosome territory.

28. (previously presented) The measurement method as set forth in Claim 10, wherein said positioning state comprises at least one of a relative position of said chromosome territory within a nucleus of said cell, a direction of a principal axis of said chromosome territory, and a spread of said chromosome territory.

29. (previously presented) The measurement method as set forth in Claim 14, wherein said positioning state comprises at least one of a relative position of said chromosome territory within a nucleus of said cell, a direction of a principal axis of said chromosome territory, and a spread of said chromosome territory.